



SEQUENCE LISTING

<110> Naoyuki TANIGUCHI et al.

<120> ALPHA 1-6 FUCOSYLTRANSFERASE

<130> 2356-7

<140> 09/839,136

<141> 2001-04-23

<150> 09/442,629

<151> 1999-11-18

<150> 08/913,805

<151> 1998-01-07

<150> PCT/JP97/00171

<151> 1997-01-23

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1728

<212> DNA

<213> Pig

<220>

<221> CDS

<222> (1)...(1728)

<400> 1

atg	cgg	cca	tgg	act	ggt	tcg	tgg	cgt	tgg	att	atg	ctc	att	ctt	ttt	48
Met	Arg	Pro	Trp	Thr	Gly	Ser	Trp	Arg	Trp	Ile	Met	Leu	Ile	Leu	Phe	
1				5					10					15		
gcc	tgg	ggg	acc	ttg	cta	ttt	tac	ata	ggt	ggt	cac	ttg	gta	cga	gat	96
Ala	Trp	Gly	Thr	Leu	Leu	Phe	Tyr	Ile	Gly	Gly	His	Leu	Val	Arg	Asp	
			20					25					30			
aat	gac	cac	tct	gat	cac	tct	agc	cga	gaa	ctg	tcc	aag	att	ttg	gca	144
Asn	Asp	His	Ser	Asp	His	Ser	Ser	Arg	Glu	Leu	Ser	Lys	Ile	Leu	Ala	
		35					40					45				
aag	ctg	gaa	cgc	tta	aaa	caa	caa	aat	gaa	gac	ttg	agg	aga	atg	gct	192
Lys	Leu	Glu	Arg	Leu	Lys	Gln	Gln	Asn	Glu	Asp	Leu	Arg	Arg	Met	Ala	
	50					55				60						
gga	tct	ctc	cga	ata	cca	gaa	ggc	ccc	att	gat	cag	ggg	cca	gct	tca	240
Gly	Ser	Leu	Arg	Ile	Pro	Glu	Gly	Pro	Ile	Asp	Gln	Gly	Pro	Ala	Ser	
65				70				75						80		
gga	aga	gtt	cgt	gct	tta	gaa	gag	caa	ttt	atg	aag	gcc	aaa	gaa	cag	288

Gly	Arg	Val	Arg	Ala	Leu	Glu	Glu	Gln	Phe	Met	Lys	Ala	Lys	Glu	Gln	
				85					90					95		
att	gaa	aat	tat	aag	aaa	caa	act	aaa	aat	ggg	cca	ggg	aag	gat	cat	336
Ile	Glu	Asn	Tyr	Lys	Lys	Gln	Thr	Lys	Asn	Gly	Pro	Gly	Lys	Asp	His	
			100					105					110			
gaa	atc	cta	agg	agg	agg	att	gaa	aat	gga	gct	aaa	gag	ctc	tgg	ttt	384
Glu	Ile	Leu	Arg	Arg	Arg	Ile	Glu	Asn	Gly	Ala	Lys	Glu	Leu	Trp	Phe	
		115					120					125				
ttt	cta	caa	agt	gag	ttg	aag	aaa	tta	aag	aat	tta	gaa	gga	aat	gaa	432
Phe	Leu	Gln	Ser	Glu	Leu	Lys	Lys	Leu	Lys	Asn	Leu	Glu	Gly	Asn	Glu	
	130					135					140					
ctc	caa	aga	cat	gca	gat	gaa	ttt	cta	tca	gat	ttg	gga	cat	cat	gaa	480
Leu	Gln	Arg	His	Ala	Asp	Glu	Phe	Leu	Ser	Asp	Leu	Gly	His	His	Glu	
145					150					155					160	
agg	tct	ata	atg	acg	gat	cta	tac	tac	ctc	agt	caa	aca	gat	ggg	gca	528
Arg	Ser	Ile	Met	Thr	Asp	Leu	Tyr	Tyr	Leu	Ser	Gln	Thr	Asp	Gly	Ala	
				165					170					175		
ggg	gat	tgg	cgt	gaa	aag	gag	gcc	aaa	gat	ctg	aca	gag	ctg	gtc	cag	576
Gly	Asp	Trp	Arg	Glu	Lys	Glu	Ala	Lys	Asp	Leu	Thr	Glu	Leu	Val	Gln	
			180					185					190			
cgg	aga	ata	aca	tat	ctt	cag	aat	ccc	aag	gac	tgc	agc	aaa	gcc	aag	624
Arg	Arg	Ile	Thr	Tyr	Leu	Gln	Asn	Pro	Lys	Asp	Cys	Ser	Lys	Ala	Lys	
		195					200					205				
aag	cta	gtg	tgt	aat	atc	aac	aaa	ggc	tgt	ggc	tat	ggc	tgt	cag	ctc	672
Lys	Leu	Val	Cys	Asn	Ile	Asn	Lys	Gly	Cys	Gly	Tyr	Gly	Cys	Gln	Leu	
	210					215					220					
cat	cat	gta	gtg	tac	tgc	ttt	atg	att	gca	tat	ggc	acc	cag	cga	aca	720
His	His	Val	Val	Tyr	Cys	Phe	Met	Ile	Ala	Tyr	Gly	Thr	Gln	Arg	Thr	
225					230					235					240	
ctc	gcc	ttg	gaa	tct	cac	aat	tgg	cgc	tac	gct	act	ggg	gga	tgg	gaa	768
Leu	Ala	Leu	Glu	Ser	His	Asn	Trp	Arg	Tyr	Ala	Thr	Gly	Gly	Trp	Glu	
				245					250					255		
act	gtg	ttt	aga	cct	gta	agt	gag	acg	tgc	aca	gac	aga	tct	ggc	agc	816
Thr	Val	Phe	Arg	Pro	Val	Ser	Glu	Thr	Cys	Thr	Asp	Arg	Ser	Gly	Ser	
			260					265					270			
tcc	act	gga	cat	tgg	tca	ggg	gaa	gta	aag	gac	aaa	aat	gtt	cag	gtg	864
Ser	Thr	Gly	His	Trp	Ser	Gly	Glu	Val	Lys	Asp	Lys	Asn	Val	Gln	Val	
		275					280					285				
gtt	gag	ctc	ccc	att	gta	gac	agt	gtt	cat	cct	cgt	cct	cca	tat	tta	912
Val	Glu	Leu	Pro	Ile	Val	Asp	Ser	Val	His	Pro	Arg	Pro	Pro	Tyr	Leu	
	290					295					300					
ccc	ctg	gct	gtc	cca	gaa	gac	ctt	gca	gat	cga	ctt	gta	cga	gtc	cat	960
Pro	Leu	Ala	Val	Pro	Glu	Asp	Leu	Ala	Asp	Arg	Leu	Val	Arg	Val	His	

305		310		315		320	
ggt gat cct gca gtg tgg tgg gta tcc cag ttt gtc aag tac ttg att							1008
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile							
		325		330		335	
cgc cca caa ccc tgg ctg gaa aag gaa ata gaa gag gcc acc aag aag							1056
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys							
		340		345		350	
cta ggc ttc aaa cat cca gtt att gga gtc cat gtt aga cgc aca gac							1104
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp							
		355		360		365	
aaa gtg gga gcg gaa gca gcc ttc cat ccc att gag gaa tac acg gtg							1152
Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val							
		370		375		380	
cac gtt gaa gaa gac ttt cag ctt ctt gct cgc aga atg caa gtg gat							1200
His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp							
		385		390		395	400
aaa aaa agg gtg tat ttg gcc aca gat gac cct gct ttg tta aaa gag							1248
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu							
		405		410		415	
gca aaa aca aag tac ccc agt tat gaa ttt att agt gat aac tct atc							1296
Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile							
		420		425		430	
tct tgg tca gct gga cta cat aat cga tat aca gaa aat tca ctt cgg							1344
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg							
		435		440		445	
ggt gtg atc ctg gat ata cac ttt ctc tcc cag gca gac ttc cta gtg							1392
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val							
		450		455		460	
tgt act ttt tca tcg cag gtc tgt aga gtt gct tat gaa atc atg caa							1440
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln							
		465		470		475	480
gcg ctg cat cct gat gcc tct gcg aac ttc cgt tct ttg gat gac atc							1488
Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile							
		485		490		495	
tac tat ttt gga ggc cca aat gcc cac aac caa att gcc att tat cct							1536
Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro							
		500		505		510	
cac caa cct cga act gaa gga gaa atc ccc atg gaa cct gga gat att							1584
His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile							
		515		520		525	
att ggt gtg gct gga aat cac tgg gat ggc tat cct aaa ggt gtt aac							1632
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn							
		530		535		540	

aga aaa ctg gga agg acg ggc cta tat ccc tcc tac aaa gtt cga gag 1680
 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
 545 550 555 560

aag ata gaa aca gtc aag tac ccc aca tat ccc gag gct gac aag taa 1728
 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys *
 565 570 575

<210> 2
 <211> 575
 <212> PRT
 <213> Pig

<400> 2
 Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
 1 5 10 15
 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
 20 25 30
 Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
 35 40 45
 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
 50 55 60
 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
 65 70 75 80
 Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
 85 90 95
 Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
 100 105 110
 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
 115 120 125
 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
 130 135 140
 Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
 145 150 155 160
 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
 165 170 175
 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
 180 185 190
 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
 195 200 205
 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
 210 215 220
 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
 225 230 235 240
 Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
 245 250 255
 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
 260 265 270
 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
 275 280 285
 Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu
 290 295 300
 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
 305 310 315 320

Gly	Asp	Pro	Ala	Val	Trp	Trp	Val	Ser	Gln	Phe	Val	Lys	Tyr	Leu	Ile
				325					330					335	
Arg	Pro	Gln	Pro	Trp	Leu	Glu	Lys	Glu	Ile	Glu	Glu	Ala	Thr	Lys	Lys
			340					345					350		
Leu	Gly	Phe	Lys	His	Pro	Val	Ile	Gly	Val	His	Val	Arg	Arg	Thr	Asp
		355					360					365			
Lys	Val	Gly	Ala	Glu	Ala	Ala	Phe	His	Pro	Ile	Glu	Glu	Tyr	Thr	Val
	370					375					380				
His	Val	Glu	Glu	Asp	Phe	Gln	Leu	Leu	Ala	Arg	Arg	Met	Gln	Val	Asp
385					390					395					400
Lys	Lys	Arg	Val	Tyr	Leu	Ala	Thr	Asp	Asp	Pro	Ala	Leu	Leu	Lys	Glu
			405					410						415	
Ala	Lys	Thr	Lys	Tyr	Pro	Ser	Tyr	Glu	Phe	Ile	Ser	Asp	Asn	Ser	Ile
			420					425					430		
Ser	Trp	Ser	Ala	Gly	Leu	His	Asn	Arg	Tyr	Thr	Glu	Asn	Ser	Leu	Arg
		435					440					445			
Gly	Val	Ile	Leu	Asp	Ile	His	Phe	Leu	Ser	Gln	Ala	Asp	Phe	Leu	Val
	450					455					460				
Cys	Thr	Phe	Ser	Ser	Gln	Val	Cys	Arg	Val	Ala	Tyr	Glu	Ile	Met	Gln
465					470					475					480
Ala	Leu	His	Pro	Asp	Ala	Ser	Ala	Asn	Phe	Arg	Ser	Leu	Asp	Asp	Ile
			485					490						495	
Tyr	Tyr	Phe	Gly	Gly	Pro	Asn	Ala	His	Asn	Gln	Ile	Ala	Ile	Tyr	Pro
			500					505					510		
His	Gln	Pro	Arg	Thr	Glu	Gly	Glu	Ile	Pro	Met	Glu	Pro	Gly	Asp	Ile
		515					520						525		
Ile	Gly	Val	Ala	Gly	Asn	His	Trp	Asp	Gly	Tyr	Pro	Lys	Gly	Val	Asn
	530					535					540				
Arg	Lys	Leu	Gly	Arg	Thr	Gly	Leu	Tyr	Pro	Ser	Tyr	Lys	Val	Arg	Glu
545					550					555					560
Lys	Ile	Glu	Thr	Val	Lys	Tyr	Pro	Thr	Tyr	Pro	Glu	Ala	Asp	Lys	
				565				570						575	

<210> 3
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 3
 Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His Glu Ile Leu Arg Arg
 1 5 10 15
 Arg Ile Glu Asn Gly Ala Lys Glu Leu Gln
 20 25

<210> 4
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 4
Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
1 5 10

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys
1 5 10

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys
1 5 10

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 9, 18
<223> n = A,T,C or G

<221> misc_feature
<222> 9, 18
<223> n = A,T,C or G

<400> 7
aarsaracna araayggncc

20

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 3, 9, 12
<223> n = A,T,C or G

<221> misc_feature
<222> 3, 9, 12
<223> n = A,T,C or G

<400> 8
tcnggrtang tnggrtaytt 20

<210> 9
<211> 2100
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (198)...(1925)

<400> 9
aagcttccta cacatatcac caggaggatc tctttgaaag attcactgca ggactaccag 60
agagaataat ttgtctgaag catcatgtgt tgaaacaaca gaagtctatt cacctgtgca 120
ctaactagaa acagagttac aatgttttca attctttgag ctccaggact ccaggggaagt 180
gagttgaaaa tctgaaa atg cgg cca tgg act ggt tcc tgg cgt tgg att 230
Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile
1 5 10

atg ctc att ctt ttt gcc tgg ggg acc ttg ctg ttt tat ata ggt ggt 278
Met Leu Ile Leu Phe Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly
15 20 25

cac ttg gta cga gat aat gac cat cct gat cac tct agc cga gaa ctg 326
His Leu Val Arg Asp Asn Asp His Pro Asp His Ser Ser Arg Glu Leu
30 35 40

tcc aag att ctg gca aag ctt gaa cgc tta aaa cag cag aat gaa gac 374
Ser Lys Ile Leu Ala Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp
45 50 55

ttg agg cga atg gcc gaa tct ctc cgg ata cca gaa ggc cct att gat 422
Leu Arg Arg Met Ala Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp
60 65 70 75

cag ggg cca gct ata gga aga gta cgc gtt tta gaa gag cag ctt gtt 470
Gln Gly Pro Ala Ile Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val
80 85 90

aag gcc aaa gaa cag att gaa aat tac aag aaa cag acc aga aat ggt 518
Lys Ala Lys Glu Gln Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly
95 100 105

ctg ggg aag gat cat gaa atc ctg agg agg agg att gaa aat gga gct 566
Leu Gly Lys Asp His Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala
110 115 120

aaa gag ctc tgg ttt ttc cta cag agt gaa ttg aag aaa tta aag aac	614
Lys Glu Leu Trp Phe Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn	
125 130 135	
tta gaa gga aat gaa ctc caa aga cat gca gat gaa ttt ctt ttg gat	662
Leu Glu Gly Asn Glu Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp	
140 145 150 155	
tta gga cat cat gaa agg tct ata atg acg gat cta tac tac ctc agt	710
Leu Gly His His Glu Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser	
160 165 170	
cag aca gat gga gca ggt gat tgg cgg gaa aaa gag gcc aaa gat ctg	758
Gln Thr Asp Gly Ala Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu	
175 180 185	
aca gaa ctg gtt cag cgg aga ata aca tat ctt cag aat ccc aag gac	806
Thr Glu Leu Val Gln Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp	
190 195 200	
tgc agc aaa gcc aaa aag ctg gtg tgt aat atc aac aaa ggc tgt ggc	854
Cys Ser Lys Ala Lys Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly	
205 210 215	
tat ggc tgt cag ctc cat cat gtg gtc tac tgc ttc atg att gca tat	902
Tyr Gly Cys Gln Leu His His Val Val Tyr Cys Phe Met Ile Ala Tyr	
220 225 230 235	
ggc acc cag cga aca ctc atc ttg gaa tct cag aat tgg cgc tat gct	950
Gly Thr Gln Arg Thr Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala	
240 245 250	
act ggt gga tgg gag act gta ttt agg cct gta agt gag aca tgc aca	998
Thr Gly Gly Trp Glu Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr	
255 260 265	
gac aga tct ggc atc tcc act gga cac tgg tca ggt gaa gtg aag gac	1046
Asp Arg Ser Gly Ile Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp	
270 275 280	
aaa aat gtt caa gtg gtc gag ctt ccc att gta gac agt ctt cat ccc	1094
Lys Asn Val Gln Val Val Glu Leu Pro Ile Val Asp Ser Leu His Pro	
285 290 295	
cgt cct cca tat tta ccc ttg gct gta cca gaa gac ctc gca gat cga	1142
Arg Pro Pro Tyr Leu Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg	
300 305 310 315	
ctt gta cga gtg cat ggt gac cct gca gtg tgg tgg gtg tct cag ttt	1190
Leu Val Arg Val His Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe	
320 325 330	
gtc aaa tac ttg atc cgc cca cag cct tgg cta gaa aaa gaa ata gaa	1238
Val Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu	
335 340 345	
gaa gcc acc aag aag ctt ggc ttc aaa cat cca gtt att gga gtc cat	1286

Glu	Ala	Thr	Lys	Lys	Leu	Gly	Phe	Lys	His	Pro	Val	Ile	Gly	Val	His		
350						355						360					
gtc	aga	cgc	aca	gac	aaa	gtg	gga	aca	gaa	gct	gcc	ttc	cat	ccc	att	1334	
Val	Arg	Arg	Thr	Asp	Lys	Val	Gly	Thr	Glu	Ala	Ala	Phe	His	Pro	Ile		
365						370						375					
gaa	gag	tac	atg	gtg	cat	gtt	gaa	gaa	cat	ttt	cag	ctt	ctt	gca	cgc	1382	
Glu	Glu	Tyr	Met	Val	His	Val	Glu	Glu	His	Phe	Gln	Leu	Leu	Ala	Arg		
380						385						390			395		
aga	atg	caa	gtg	gac	aaa	aaa	aga	gtg	tat	ttg	gcc	aca	gat	gac	cct	1430	
Arg	Met	Gln	Val	Asp	Lys	Lys	Arg	Val	Tyr	Leu	Ala	Thr	Asp	Asp	Pro		
			400						405						410		
tct	tta	tta	aag	gag	gca	aaa	aca	aag	tac	ccc	aat	tat	gaa	ttt	att	1478	
Ser	Leu	Leu	Lys	Glu	Ala	Lys	Thr	Lys	Tyr	Pro	Asn	Tyr	Glu	Phe	Ile		
			415						420						425		
agt	gat	aac	tct	att	tcc	tgg	tca	gct	gga	ctg	cac	aat	cga	tac	aca	1526	
Ser	Asp	Asn	Ser	Ile	Ser	Trp	Ser	Ala	Gly	Leu	His	Asn	Arg	Tyr	Thr		
			430						435						440		
gaa	aat	tca	ctt	cgt	gga	gtg	atc	ctg	gat	ata	cat	ttt	ctc	tct	cag	1574	
Glu	Asn	Ser	Leu	Arg	Gly	Val	Ile	Leu	Asp	Ile	His	Phe	Leu	Ser	Gln		
			445						450						455		
gca	gac	ttc	cta	gtg	tgt	act	ttt	tca	tcc	cag	gtc	tgt	cga	gtt	act	1622	
Ala	Asp	Phe	Leu	Val	Cys	Thr	Phe	Ser	Ser	Gln	Val	Cys	Arg	Val	Thr		
460						465						470			475		
tat	gaa	att	atg	caa	aca	cta	cat	cct	gat	gcc	tct	gca	aac	ttc	cat	1670	
Tyr	Glu	Ile	Met	Gln	Thr	Leu	His	Pro	Asp	Ala	Ser	Ala	Asn	Phe	His		
			480						485						490		
tct	tta	gat	gac	atc	tac	tat	ttt	ggg	ggc	cag	aat	gcc	cac	aat	caa	1718	
Ser	Leu	Asp	Asp	Ile	Tyr	Tyr	Phe	Gly	Gly	Gln	Asn	Ala	His	Asn	Gln		
			495						500						505		
att	gcc	att	tat	gct	cac	caa	ccc	cga	act	gca	gat	gaa	att	ccc	atg	1766	
Ile	Ala	Ile	Tyr	Ala	His	Gln	Pro	Arg	Thr	Ala	Asp	Glu	Ile	Pro	Met		
			510						515						520		
gaa	cct	gga	gat	atc	att	ggg	gtg	gct	gga	aat	cat	tgg	gat	ggc	tat	1814	
Glu	Pro	Gly	Asp	Ile	Ile	Gly	Val	Ala	Gly	Asn	His	Trp	Asp	Gly	Tyr		
			525						530						535		
tct	aaa	ggg	gtc	aac	agg	aaa	ttg	gga	agg	acg	ggc	cta	tat	ccc	tcc	1862	
Ser	Lys	Gly	Val	Asn	Arg	Lys	Leu	Gly	Arg	Thr	Gly	Leu	Tyr	Pro	Ser		
540						545						550			555		
tac	aaa	gtt	cca	gag	aag	ata	gaa	acg	gtc	aag	tac	ccc	aca	tat	cct	1910	
Tyr	Lys	Val	Pro	Glu	Lys	Ile	Glu	Thr	Val	Lys	Tyr	Pro	Thr	Tyr	Pro		
			560						565						570		
gag	gct	gag	aaa	taa	agctcacatg	gaagagataa				acgaccaaac				tcagttcgac		1965	
Glu	Ala	Glu	Lys	*													

575

caaactcagt tcaaaccatt tcagccaaac tgtagatgaa gagggctctg atctaacaaa 2025
 ataagggttat atgagtagat actctcagca ccaagagcag ctgggaactg acataggctt 2085
 caattggtgg aattc 2100

<210> 10
 <211> 575
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
 1 5 10 15
 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
 20 25 30
 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
 35 40 45
 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
 50 55 60
 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile
 65 70 75 80
 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
 85 90 95
 Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His
 100 105 110
 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
 115 120 125
 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
 130 135 140
 Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu
 145 150 155 160
 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
 165 170 175
 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
 180 185 190
 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
 195 200 205
 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
 210 215 220
 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
 225 230 235 240
 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
 245 250 255
 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile
 260 265 270
 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
 275 280 285
 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
 290 295 300
 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
 305 310 315 320
 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
 325 330 335
 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
 340 345 350
 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp

<210> 13
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser
1 5 10

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
ttyaarcayc chgtbatygg 20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gwrtrtrtcrgr wratraaytc 20